RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/828,831_

Source: _IPWO_

Date Processed by STIC: _09-28-2005_

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IFWO

RAW SEQUENCE LISTING   DATE: 09/28/2005
PATENT APPLICATION: US/10/828,831   TIME: 07:54:40

Input Set : N:\Crf3\RULE60\10828831.raw.txt
Output Set: N:\CRF4\09282005\J828831.raw

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 1 <110> APPLICANT: EVANS, RONALD M.
 2        NO, DAVID
 3        SAEZ, ENRIQUE
 4 <120> TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
 5        MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO
 6 <130> FILE REFERENCE: SALK1520-2
 7 <140> CURRENT APPLICATION NUMBER: US/10/828,831
 8 <141> CURRENT FILING DATE: 2004-04-20
 9 <150> PRIOR APPLICATION NUMBER: US/09/042,488
10 <151> PRIOR FILING DATE: 1998-03-16
11 <150> PRIOR APPLICATION NUMBER: 08/974,530
12 <151> PRIOR FILING DATE: 1997-11-19
13 <150> PRIOR APPLICATION NUMBER: 08/628,830
14 <151> PRIOR FILING DATE: 1996-04-05
15 <160> NUMBER OF SEQ ID NOS: 18
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 71
20 <212> TYPE: PRT
21 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
24        peptide sequence
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     26 <222> LOCATION: (2)..(3)
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     30 <223> OTHER INFORMATION: Any amino acid
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     32 <222> LOCATION: (8)
     33 <223> OTHER INFORMATION: Any amino acid
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     35 <222> LOCATION: (10)
     36 <223> OTHER INFORMATION: Any amino acid
W--> 37 <221> MOD_RES
     38 <222> LOCATION: (12)
     39 <223> OTHER INFORMATION: Any amino acid
W--> 40 <221> MOD_RES
     41 <222> LOCATION: (14)..(17)
     42 <223> OTHER INFORMATION: Any amino acid
W--> 43 <221> MOD_RES
     44 <222> LOCATION: (19)..(20)
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Input Set : N:\Crf3\RULE60\10828831.raw.txt
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W--> 46 <221> MOD_RES
       47 <222> LOCATION: (23)
       48 <223> OTHER INFORMATION: Any amino acid
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       50 <222> LOCATION: (26)
       51 <223> OTHER INFORMATION: Any amino acid
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       53 <222> LOCATION: (28)..(38)
       54 <223> OTHER INFORMATION: Any amino acid
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       56 <222> LOCATION: (40)..(47)
       57 <223> OTHER INFORMATION: Any amino acid
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       59 <222> LOCATION: (49)..(51)
       60 <223> OTHER INFORMATION: Any amino acid
W--> 61 <221> MOD_RES
       62 <222> LOCATION: (53)..(54)
       63 <223> OTHER INFORMATION: Any amino acid
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       65 <222> LOCATION: (56)..(57)
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       72 <223> OTHER INFORMATION: Any amino acid
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       74 <222> LOCATION: (67)..(69)
       75 <223> OTHER INFORMATION: Any amino acid
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W--> 77       Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
       78       1               5               10              15
       79       Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
       80                   20              25              30
       81       Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
       82                   35              40              45
       83       Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
       84             50              55              60
       85       Lys Cys Xaa Xaa Xaa Gly Met
       86       65                  70
       88 <210> SEQ ID NO: 2
       89 <211> LENGTH: 5
       90 <212> TYPE: PRT
       91 <213> ORGANISM: Artificial Sequence
       92 <220> FEATURE:
       93 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 99 <210> SEQ ID NO: 3
100 <211> LENGTH: 5
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
105       peptide
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107       Gly Ser Cys Lys Val
108        1               5
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 2241
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: Recombinant
116       VgEcR
117 <221> NAME/KEY: CDS
118 <222> LOCATION: (1)..(2238)
119 <400> 4
120       atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac    48
121       Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
122        1               5                  10                  15
123       ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat    96
124       Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
125                      20                  25                  30
126       ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc   144
127       Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
128                      35                  40                  45
129       cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt   192
130       His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
131              50                  55                  60
132       gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag   240
133       Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
134           65                  70                  75                  80
135       ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc   288
136       Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
137                      85                  90                  95
138       gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa   336
139       Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
140                     100                 105                 110
141       agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa   384
142       Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
143                     115                 120                 125
144       gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac   432
145       Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
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146          130                    135                    140
147     aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt    480
148     Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
149     145                    150                    155                    160
150     acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg    528
151     Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
152                         165                    170                    175
153     gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc    576
154     Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
155                         180                    185                    190
156     ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt    624
157     Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
158                    195                    200                    205
159     gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg    672
160     Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
161          210                    215                    220
162     acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct    720
163     Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
164     225                    230                    235                    240
165     ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca    768
166     Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
167                         245                    250                    255
168     tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata    816
169     Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
170                         260                    265                    270
171     ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag    864
172     Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
173                    275                    280                    285
174     ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag    912
175     Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
176          290                    295                    300
177     cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac    960
178     Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
179     305                    310                    315                    320
180     gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata    1008
181     Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
182                         325                    330                    335
183     ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt    1056
184     Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
185                         340                    345                    350
186     aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg    1104
187     Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
188                    355                    360                    365
189     tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg    1152
190     Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
191          370                    375                    380
192     gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac    1200
193     Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
194     385                    390                    395                    400
```

```
195    aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc    1248
196    Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
197                405                     410                     415
198    cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc    1296
199    Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
200                420                     425                     430
201    act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa    1344
202    Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
203                435                     440                     445
204    cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat    1392
205    Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
206                450                     455                     460
207    ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca    1440
208    Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
209    465                     470                     475                     480
210    aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac    1488
211    Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
212                485                     490                     495
213    gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag    1536
214    Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
215                500                     505                     510
216    ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag    1584
217    Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
218                515                     520                     525
219    tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct    1632
220    Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
221                530                     535                     540
222    gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat    1680
223    Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
224    545                     550                     555                     560
225    tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag    1728
226    Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
227                565                     570                     575
228    cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat    1776
229    Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
230                580                     585                     590
231    tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag    1824
232    Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
233                595                     600                     605
234    ctg caa ggt caa ctg caa ccc cag ctc caa cca cag ctt cag acg caa    1872
235    Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
236                610                     615                     620
237    ctc cag cca cag att caa cca cag cca cag ctc ctt ccc gtc tcc gct    1920
238    Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
239    625                     630                     635                     640
240    ccc gtg ccc gcc tcc gta acc gca cct ggt tcc ttg tcc gcg gtc agt    1968
241    Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
242                645                     650                     655
243    acg agc agc gaa tac atg ggc gga agt gcg gcc ata gga ccc atc acg    2016
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<pre>
RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/28/2005
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      Input Set : N:\Crf3\RULE60\10828831.raw.txt
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</pre>

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

<pre>
Seq#:1; Xaa Pos. 2,3,5,6,8,10,12,14,15,16,17,19,20,23,26,28,29,30,31,32,33
Seq#:1; Xaa Pos. 34,35,36,37,38,40,41,42,43,44,45,46,47,49,50,51,53,54,56
Seq#:1; Xaa Pos. 57,59,60,63,64,67,68,69
Seq#:10; N Pos. 4,5,7,8,9,10,11,14,15
Seq#:11; N Pos. 3,4,7,8,9,10,11,13,14
Seq#:12; N Pos. 7
Seq#:13; N Pos. 4,5,7,8,9,10,11,15,16
</pre>

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

<pre>
Seq#:1; Line(s) 4
Seq#:10; Line(s) 980
Seq#:11; Line(s) 1001
Seq#:13; Line(s) 1035
</pre>

VERIFICATION SUMMARY   DATE: 09/28/2005
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Input Set : N:\Crf3\RULE60\10828831.raw.txt
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L:25  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:28  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:31  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:34  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:46  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:49  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:52  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:55  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:58  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:61  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:64  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:67  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:70  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:73  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:76  M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:77  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:117 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:119 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:372 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:374 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:627 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:629 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:975 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:978 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:983 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:986 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:996 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:999 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1004 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1007 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1017 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1020 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1030 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1033 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1038 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
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